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(54) Title: METHOD FOR THE DETECTION OF SPECIFIC NUCLEIC ACID SEQUENCES BY POLYMERASE NUCLEOTIDE INCORPORATION			
(57) Abstract			
<p>A method for rapid and efficient detection of a target DNA or RNA sequence is provided. A primer having a 3'-hydroxyl group at one end and having a sequence of nucleotides sufficiently homologous with an identifying sequence of nucleotides in the target DNA is selected. The primer is hybridized to the identifying sequence of nucleotides on the DNA or RNA sequence and a reporter molecule is synthesized on the target sequence by progressively binding complementary nucleotides to the primer, where the complementary nucleotides include nucleotides labeled with a fluorophore. Fluorescence emitted by fluorophores on single reporter molecules is detected to identify the target DNA or RNA sequence.</p>			

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METHOD FOR THE DETECTION OF SPECIFIC NUCLEIC ACID SEQUENCES BY POLYMERASE NUCLEOTIDE INCORPORATION

RELATED APPLICATION

This application claims the benefit of U.S. Provisional Application S.N. 60/113,139, filed December 18, 1999.

5

STATEMENT REGARDING FEDERAL RIGHTS

This invention was made with government support under Contract No. W-7405-ENG-36 awarded by the U.S. Department of Energy. The government has certain rights in the invention.

10

FIELD OF THE INVENTION

The present invention relates generally to detection of nucleic acid sequences, and, more particularly, to the selective incorporation of fluorescent markers to detect nucleic acid sequences.

15

BACKGROUND OF THE INVENTION

The rapid and efficient detection of specific nucleic acid sequences in biological samples plays a central role in a variety of fields, including molecular biology, biotechnology, immunology, medical diagnosis, forensic analysis, and quality control of food products. One of the most commonly used techniques for the 20 detection of specific nucleic acid sequences is the Southern blot. This is a hybridization technique in which the fragments to be interrogated have been size-separated by gel electrophoresis and transferred from the gel to a nylon nitrocellulose filter. A radioactive probe is then added to the filter so that hybridization takes place. After washing away the excess probe, the band 25 containing the target nucleic acid is detected by exposing an x-ray film to the filter.

Despite its popularity, Southern blotting suffers from some limitations: it

involves a series of manually intensive procedures that cannot be run unattended and cannot be readily automated. The process for separating the fragments by gel electrophoresis and subsequently detecting the bands by autoradiography are time-consuming tasks that are susceptible to poor quantitative accuracy and poor
5 reproducibility.

The use of radioactive probes brings up a set of safety and environmental concerns. The lack of adequate sensitivity is another limitation, which has been partially addressed by the development of the polymerase chain reaction (PCR) and related target amplification methods. The PCR consists of selectively amplifying a
10 target DNA sequence in a sample. Amplification products are usually detected by dyes that stain nucleic acids or by hybridization with sequence-specific probes. Amplification methods, however, may introduce ambiguities resulting from
15 contamination or from variability in amplification efficiency. Therefore, there is a need for robust analytical methods that provide accurate quantitation and molecular weight estimates for target DNA or RNA segments.

Various objects, advantages and novel features of the invention will be set forth in part in the description which follows, and in part will become apparent to those skilled in the art upon examination of the following or may be learned by practice of the invention. The objects and advantages of the invention may be
20 realized and attained by means of the instrumentalities and combinations particularly pointed out in the appended claims.

SUMMARY OF THE INVENTION

To achieve the foregoing and other objects, and in accordance with the
25 purposes of the present invention, as embodied and broadly described herein, the present invention includes a method for identifying a target DNA or RNA sequence. A primer having a 3'-hydroxyl group at one end and having a sequence of nucleotides sufficiently homologous to hybridize with an identifying sequence of nucleotides in the target DNA or RNA is selected. The primer is hybridized to the
30 identifying sequence of nucleotides and a reporter molecule is synthesized on the target sequence by extending the primer by progressively binding nucleotides to the

primer that are complementary to the corresponding nucleotides of the DNA or RNA sequence, where the complementary nucleotides include nucleotides labeled with a fluorophore. Fluorescence emitted by fluorophores on individual reporter molecules is detected to identify the target DNA or RNA sequence.

5

BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying drawings, which are incorporated in and form a part of the specification, illustrate embodiments of the present invention and, together with the description, serve to explain the principles of the invention. In the drawings:

10 FIGURES 1A-1E schematically depict the process of the present invention.

FIGURE 2 graphically depicts the experimental results for the detection of a specific sequence of pUC19 DNA at the single-molecule level of sensitivity according to one embodiment of the present invention.

15 FIGURE 3 graphically depicts results for a control experiment run under identical conditions as those corresponding to the experimental results shown in FIGURE 2, except that the target was replaced by lambda DNA.

FIGURE 4 graphically depicts a simulation of single molecule fluorescence signals from a reporter molecule according to a second embodiment of the present invention.

20

DETAILED DESCRIPTION

In accordance with the present invention, a new method enables the direct detection of specific nucleic acid sequences in biological samples. The basis of the approach is to monitor for the presence of a specific nucleic acid sequence of 25 bacterial, human, plant or other origin. The nucleic acid sequence may be a DNA or RNA sequence, and may be characteristic of a specific taxonomic group, a specific physiological function, or a specific genetic trait.

The method consists of synthesizing in vitro a fluorescent nucleic acid reporter molecule using a relatively short sequence of the target as a template as 30 shown in Figures 1A-1E. A DNA target (Figure 1A) is denatured according to well known processes to form a single stranded DNA target (Figure 1B). A short

oligonucleotide primer that is specific and complementary to the target is then hybridized to the single stranded DNA target. A suitable polymerase and free nucleotides are added to the sample. One of these oligonucleotides is at least partially labeled with a fluorophore. If the target is present in the sample, the primer
5 binds to an identifying sequence of the target, (Figure 1C) and the polymerase will incorporate the labeled and unlabeled nucleotides (Figure 1D) to reconstruct the target's complementary sequence as shown in Figure 1E. If the labeled nucleotide concentration is kept below that of the unlabeled nucleotides, most of the labeled nucleotides will be incorporated into the reporter DNA molecule. Nonetheless,
10 some free (i.e., unbound) labeled nucleotides will remain in the reaction mixture, but fluorescence from each synthesized reporter molecule will be much stronger than that of the free nucleotide background over the single-molecule detection time.

The sample is analyzed in a single molecule detection apparatus, as are well known and described in the art. Detection of the synthesized reporter molecule
15 signifies the presence of the target being sought. The fluorescent signal from the reporter molecule is much larger than that of the background fluorescence originating from free labeled nucleotides, since the reaction is allowed to proceed until the reporter molecule is hundreds or thousands of bases long. The new method described here combines the advantages of flow-based analytical systems
20 (system automation, speed, reproducibility) with the unsurpassed sensitivity of single-molecule detection. The sensitivity of this method allows for the direct detection of specific genes without the need for using amplification methods such as PCR and exhibits advantages over current methodologies in terms of sensitivity, speed and per-assay-cost. The non-radioactive approach for the ultrasensitive
25 detection of specific sequences described here has applications in a wide variety of fields, such as gene identification, gene mapping, medical diagnostics, and biotechnology.

Exemplary Process

30 As an example, experiments were performed for the detection of pUC19 DNA, (a 2686 base-pair plasmid). Prior to all experiments, pUC19 DNA was

digested with the restriction endonuclease Bgl I, which yields two fragments, 1568 bp and 1118 bp in length. As a control, identical experiments were run except that pUC19 DNA was substituted with lambda DNA. A specific sequence of the 1568-bp pUC19 fragment was detected at the single-molecule level of sensitivity. The 5 lambda DNA control yielded negative results.

a. Primer design. Primer sequences should be specific to the target being sought. Primers are typically 15-30 nucleotides long. Primer lengths greater than 15 nucleotides ensure that they will not anneal specifically to non-target nucleic 10 acid. Generally, primer sequences have the following characteristics:

1. No internal secondary structures that impede hybridization and extension.
2. Balanced distribution of G/C and A/T rich domains (45-55%).
3. For the example experiment, we used the following 24-mer primer, which anneals to nucleotides 352-375 of pUC19:

15 5'-d(CGC-CAG-GGT-TTT-CCC-AGT-CAC-GAC)-3' (SEQ ID 1)

b. Nucleic acid extraction and isolation. Common extraction methods, such as phenol extraction, can be used to isolate the DNA from the sample under investigation. See, for example, Reference 1 for nucleic acid extraction protocols.

c. Reporter synthesis.

i. Reagents:

Name	Initial Conc.	Volume	Final Concentration	Source
Buffer	10X	5 uL	1.0X	Promega Core System II cat. # M7665
pUC19 DNA (2686 bp) digestion product (diluted 1:25)	40ng/uL	4 uL	3.2ng/uL (160ng/50uL) 1.83 E-9 M	N.E. Biolabs cat. # 304-1S
Primer	10ng/uL 1.26pmol/uL	4 uL	0.1 uM (5 pmol)	Promega cat. # Q5601
Nucleotide mixture DATP DCTP DGTP DTTP Bodipy-TMR-14-dUTP	1 mM 1 mM 1 mM 0.8 mM 0.2 mM	1 uL	20 uM each	Promega cat # U1330 Promega cat # U1330 Promega cat # U1330 Promega cat # U1330 Molecular Probes cat. # C-7616
Taq polymerase	5u/uL	0.25 uL	1.25u/50uL	Promega Core System II
MgCl ₂	25mM	3 uL	1.5 mM	Promega Core System II
Distilled Water		Complete to 50uL		

5 ii. Denature target DNA at 95°C for 5 minutes.

iii. Mix all reagents gently and thoroughly. Add enzyme last. Centrifuge briefly to collect sample at bottom of tube.

10 iv. Extension: Incubate at 72°C for 3 hours.

A proper temperature is selected for the hybridization of dNTP to extend the primer along the target DNA molecule. If the temperature is too low, non-specific annealing will increase. An optimal hybridization temperature may be predicted for a given primer/target pair with available software routines, e.g., PRIMER, developed by The Whitehead Institute for Biomedical

Research. For this example, the optimal temperature for Taq DNA polymerase activity is 72° C.

5 v. Optional: Add "STOP" solution to terminate enzymatic activity. If the reaction is not stopped, and the target is of suitable size, the amount of incorporated dye and, therefore, the reporter fluorescence intensity, will be proportional to the size of the fragment.

10 vi. Optional: remove free, unincorporated labeled nucleotides by physical means (e.g., precipitation, filtration, chromatography). In the exemplary results reported herein, a large fraction of the unincorporated labeled nucleotides were removed using a QIAquick Nucleotide Removal Kit (Quagen, Valencia, CA) following the manufacturer's protocols. Conversely, the primer can be labeled with a suitable immobilization group (e.g., biotin), which allows isolation of the reporter by physical means (e.g., solid support, 15 magnetic beads).

d. Analysis by single-molecule detection.

20 A single-molecule detection apparatus such as a variation of that described in References 2 and 3 or U.S. Patent 5,209,834, issued May 11, 1993, is used to detect fluorescence from the reporter molecule. Suitable flow cytometer apparatus and methods for single molecule detection are found in U.S. Patent 5,558,998, issued September 24, 1996, and U.S. Patent Application 09/169,025, filed October 9, 1998, both incorporated by reference. Depending on reaction conditions, such as initial nucleotide concentration and temperature, it may or may not be necessary to remove 25 unincorporated labeled nucleotide as explained in the Procedure section. In this example, the reaction mixture was diluted 1000-fold to 50 mL. This dilution yields a concentration of unincorporated nucleotide in the nanomolar range, and a concentration of reporter in the picomolar range. Therefore, when the sample is analyzed by single-molecule detection, the 30 unincorporated nucleotide produces a constant background signal, and the reporter, which contains hundreds of labels, produces single fluorescence

bursts with amplitudes well above that of the background. Figure 2 shows the experimental results for the detection of pUC19 in this example. Figure 3 shows the control experiments using lambda DNA as target.

If the reporter synthesis reaction is allowed to proceed to completion,
5 the amount of labeled nucleotide that is incorporated will be the same for identical targets. Therefore, each single-molecule burst will present the same amplitude, as shown in the simulation of Figure 4.

e. Analysis by single-molecule electrophoresis.

Another way to avoid detecting interfering free nucleotides is to
10 perform "single-molecule electrophoresis" as described in Reference 3 and in U.S. Patent 5,209,834, incorporated by reference. In this method, the electrophoretic mobility of fluorescently labeled molecules (free labeled nucleotides and reporter molecules in this case) can be determined with single-molecule sensitivity. Since single nucleotides exhibit an
15 electrophoretic mobility vastly different to that of nucleic acid targets, interference from free nucleotides is eliminated. Therefore, each single-molecule burst will present the same amplitude, as shown in the simulation of Figure 4. A histogram of burst amplitudes will reveal the size of the target being sought. This method also allows a determination of the size of the
20 target, even if the reaction was not allowed to complete.

References (incorporated herein by reference)

1. "DNA Probes", G. Keller and M. Manak, Stockton Press, New York, 1993, section 2.
2. "Single-molecule detection of specific nucleic acid sequences in unamplified genomic DNA", A. Castro and J.G.K. Williams, *Anal. Chem.* 69, 3915-3920 (1997).
- 25 3. "Single-Molecule Electrophoresis". A. Castro and E. B. Shera, *Anal. Chem.* 67, 3181 (1995).

The foregoing description of the invention has been presented for purposes
30 of illustration and description and is not intended to be exhaustive or to limit the

invention to the precise form disclosed, and obviously many modifications and variations are possible in light of the above teaching.

The embodiments were chosen and described in order to best explain the principles of the invention and its practical application to thereby enable others 5 skilled in the art to best utilize the invention in various embodiments and with various modifications as are suited to the particular use contemplated. It is intended that the scope of the invention be defined by the claims appended hereto.

WHAT IS CLAIMED IS:

1. A method for identifying a target DNA or RNA sequence comprising the steps of:

selecting a primer having a 3'-hydroxyl group at one end and having a sequence of nucleotides sufficiently homologous to hybridize with an identifying sequence of nucleotides in the target DNA;

5

hybridizing the primer to the identifying nucleotide sequences of the target DNA or RNA sequence;

10 extending the primer along the target sequence by progressively binding nucleotides to the primer that are complementary to the corresponding nucleotides on the target sequence to form a reporter molecule, where the complementary nucleotides include nucleotides labeled with a fluorophore; and

detecting fluorescence emitted by fluorophores on individual reporter molecules to identify the target DNA or RNA sequence.

2. A method according to Claim 1, wherein the primer is at least about 15 nucleotides to specifically hybridize to the identifying sequence of nucleotides for the target DNA or RNA.

3. A method according to Claim 1, including the steps of:

forming a mixture of dATP, dGTP, dCTP, and dUTP nucleotides, where at least one of the nucleotide types is at least partially labeled with a fluorescent label;

denaturing the target DNA or RNA;

5 adding a polymerase effective to catalyze the synthesis of the reporter molecule from the mixture of nucleotides; and

incubating the mixture of nucleotides, target DNA or RNA, and polymerase for a time effective to extend the primer to a desired length.

4. A method according to Claim 3, wherein the concentration of nucleotides in the mixture of nucleotides having a fluorescent label is less than the concentration of nucleotides without a fluorescent label.

5. A method according to Claim 1, further including the step of removing free, unincorporated nucleotides after the binding reaction is completed.

6. A method according to Claim 5, wherein the primer is at least about 15 nucleotides to specifically hybridize to the identifying sequence of nucleotides for the target DNA or RNA.

7. A method according to Claim 5, including the steps of:
forming a mixture of dATP, dGTP, dCTP, and dUTP nucleotides, where at least one of the nucleotide types is at least partially labeled with a fluorescent label;
denaturing the target DNA or RNA;
5 adding a polymerase effective to catalyze the synthesis of the reporter molecule from the mixture of nucleotides; and
incubating the mixture of nucleotides, target DNA or RNA, and polymerase for a time effective to extend the primer to a desired length.

8. A method according to Claim 7, wherein the concentration of nucleotides in the mixture of nucleotides having a fluorescent label is less than the concentration of nucleotides without a fluorescent label.

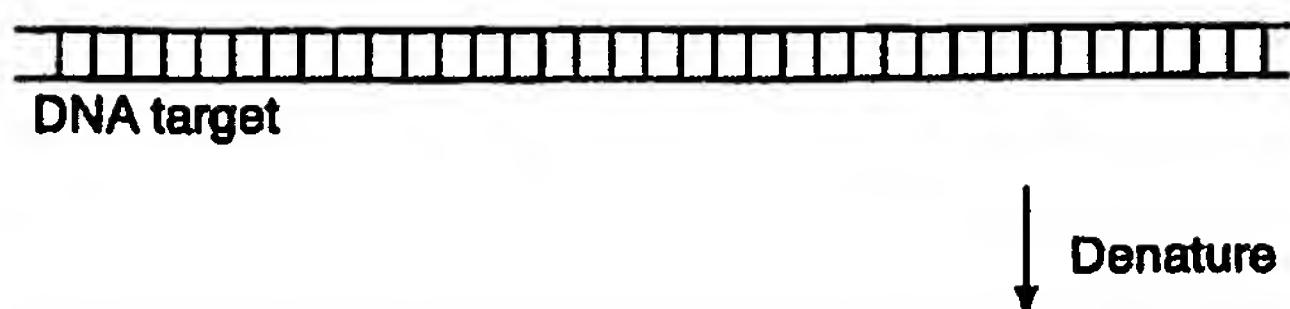
9. A method according to Claim 1, further including the step of separating free, unincorporated nucleotides from reporter molecules by single-molecule electrophoresis.

10. A method according to Claim 9, wherein the primer is at least about 15 nucleotides to specifically hybridize to the identifying sequence of nucleotides for the target DNA or RNA.

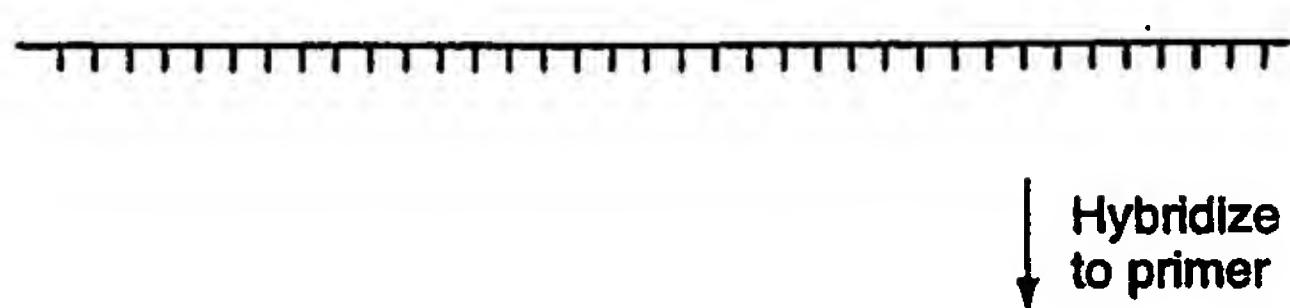
11. A method according to Claim 9, including the steps of:
 - forming a mixture of dATP, dGTP, dCTP, and dUTP nucleotides, where at least one of the nucleotide types is at least partially labeled with a fluorescent label;
 - denaturing the target DNA or RNA;
 - 5 adding a polymerase effective to catalyze the synthesis of the reporter molecule from the mixture of nucleotides; and
 - incubating the mixture of nucleotides, target DNA or RNA, and polymerase for a time effective to extend the primer to a desired length.

12. A method according to Claim 11, wherein the concentration of nucleotides in the mixture of nucleotides having a fluorescent label is less than the concentration of nucleotides without a fluorescent label.

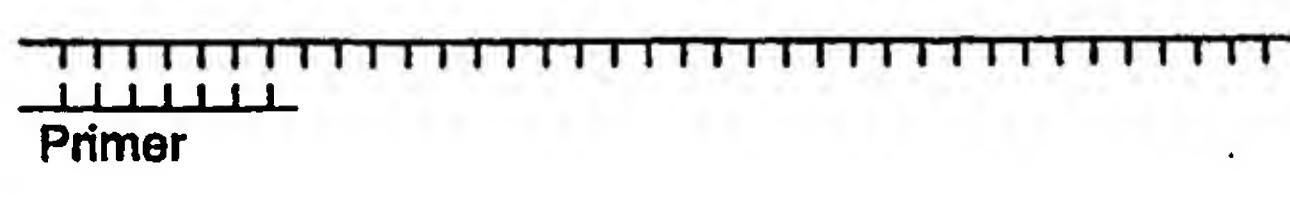
1/3

**Fig. 1A**

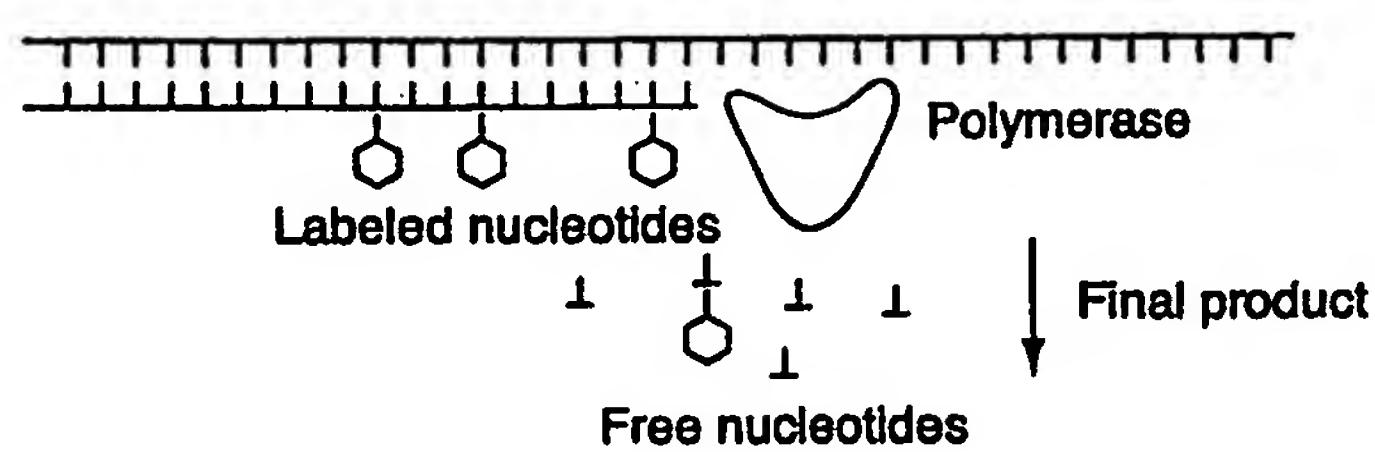
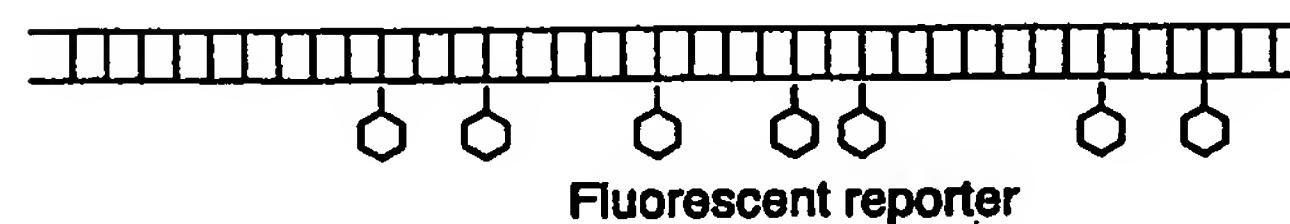
↓ Denature

**Fig. 1B**

↓ Hybridize to primer

**Fig. 1C**

↓ Extend using polymerase

**Fig. 1D****Fig. 1E**

2/3

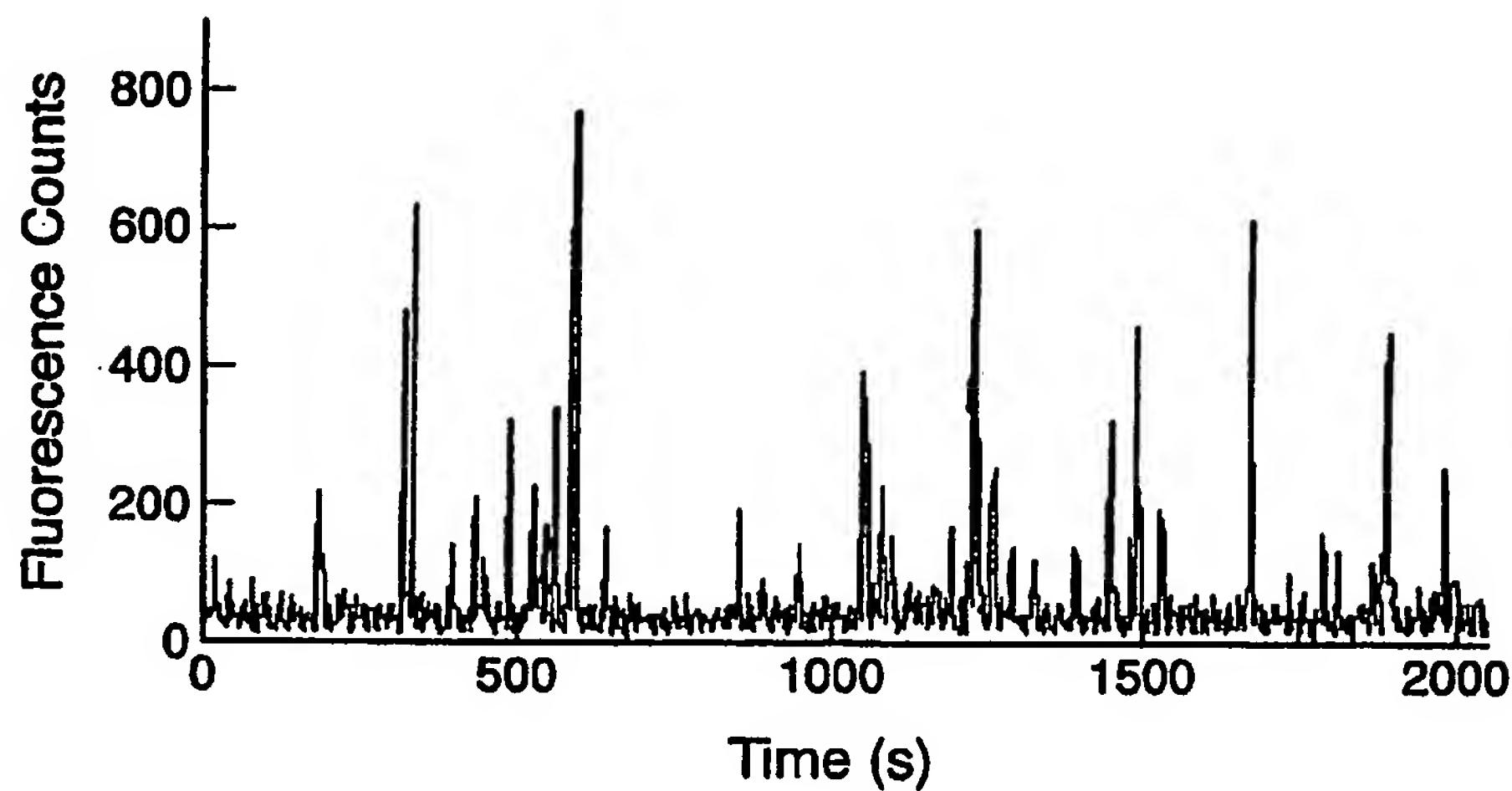


Fig. 2

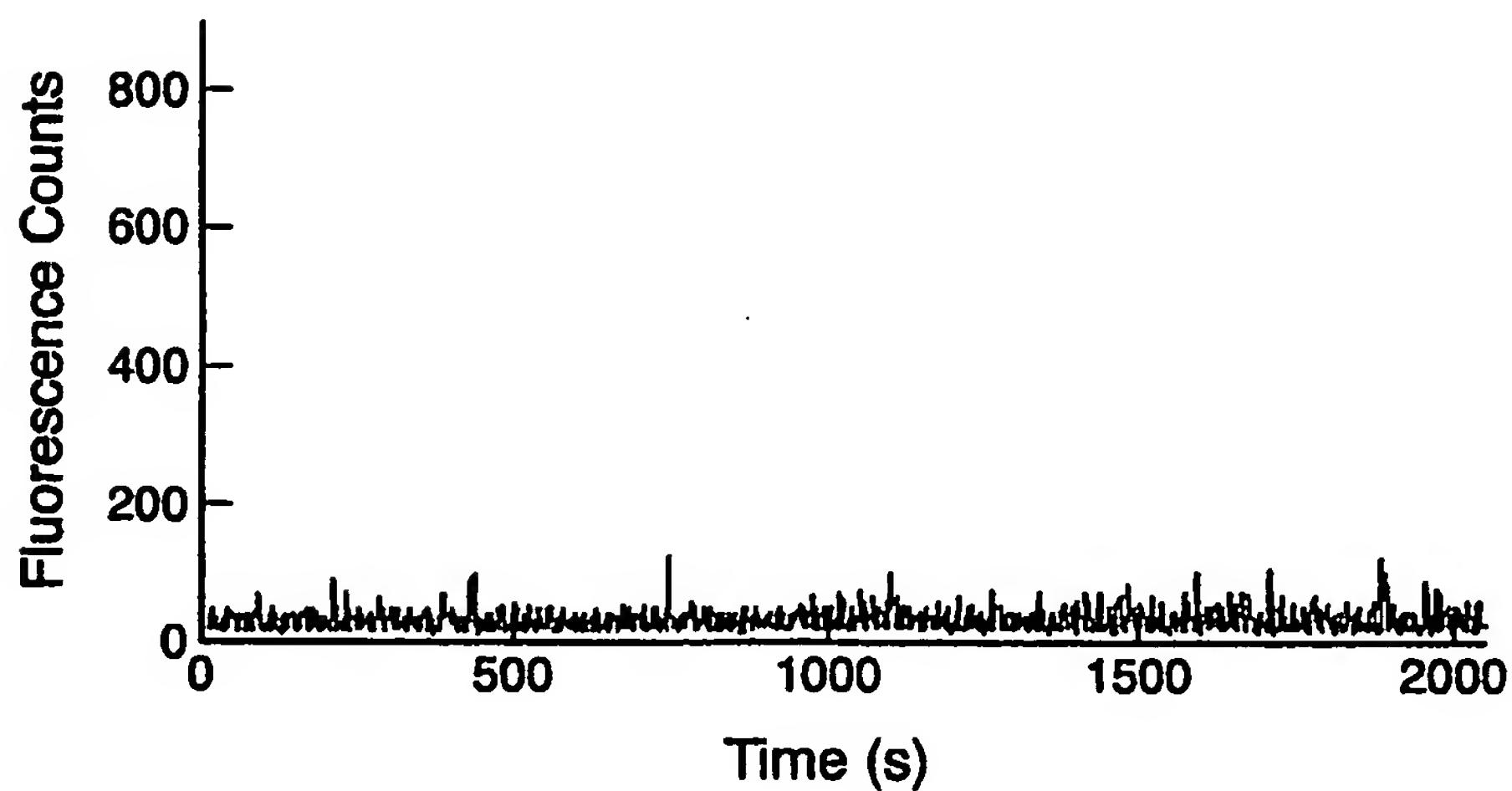


Fig. 3

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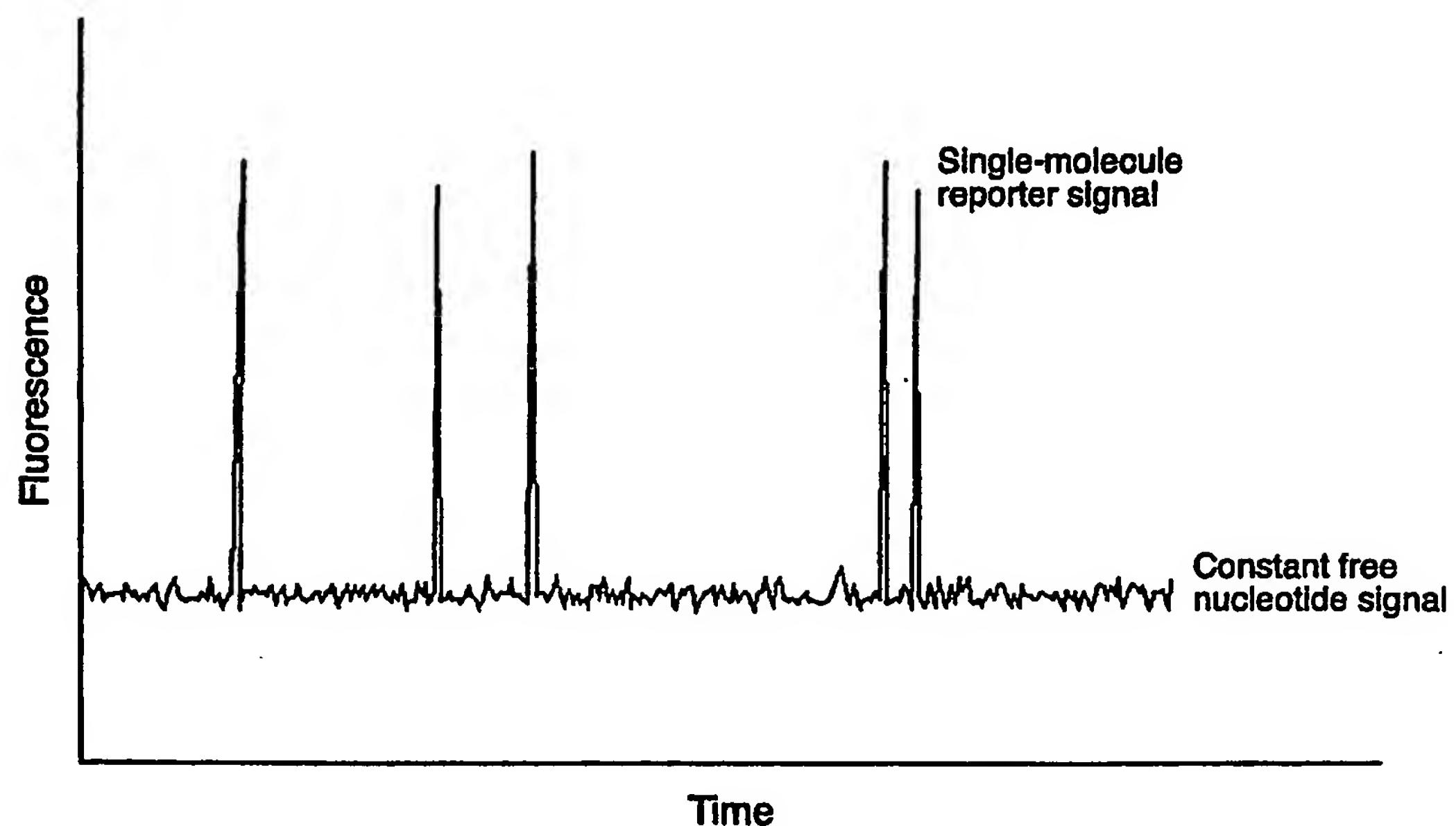


Fig. 4

1

SEQUENCE LISTING

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"

"
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"

"
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"

"
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"

"
<213> pUC19
"

"
<400> 1
"

cgccagggtt ttcccaagtca cgac

24

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/28612

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :C12Q 1/68; C12P 19/34; C12N 15/00; C07H 21/04
 US CL : 435/6, 91.1, 91.2; 536/ 24.33, 25.3, 25.32, 23.1, 24.3

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1, 91.2; 536/ 24.33, 25.3, 25.32, 23.1, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, E	US 6,004,744 A (GOELET et al) 21 December 1999, column 9, lines 26-31 and 55-56, column 10, lines 35-63 and Examples 3-4.	1-12
Y	US 5,518,900 A (NIKIFOROV et al) 21 May 1996, see entire patent, especially starting at column 8.	1-12
Y	US 4,683,195 A (MULLIS et al) 28 July 1987, column 38, lines 30-43, column 37, lines 15-20.	1-12

Further documents are listed in the continuation of Box C. See patent family annex.

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•L• document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	•Y•	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
•O• document referring to an oral disclosure, use, exhibition or other means	•&•	document member of the same patent family
•P• document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CHANG, H. In Situ transcription with Tth DNA polymerase and fluorescent nucleotides. Journal of Immunological Methods. July 1994, Volume 176, No. 2, page 236, column 2, lines 38-42, page 240, column 1, lines 13 and 14.	1-12

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/28612

B FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

West 1.2, STN express, Medline, Scisearch, Embase, Biosis

Search terms: primer, hydroxyl group, nucleic acid, DNA, RNA, target, extend, extending, label, fluorescent, fluorophore, polymerase, deoxynucleotide triphosphates, amplification, PCR, nucleotides, hybridize, complementary